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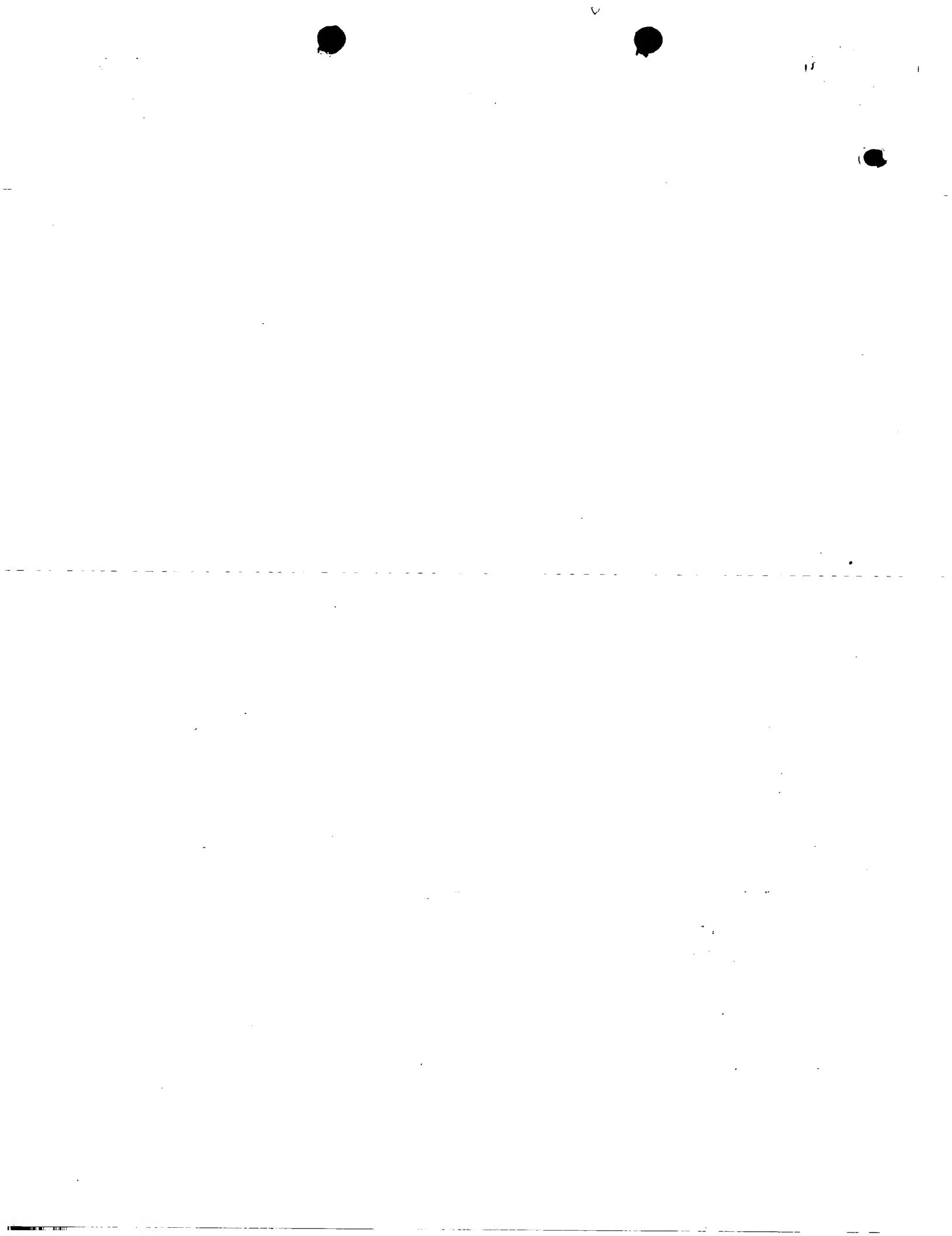
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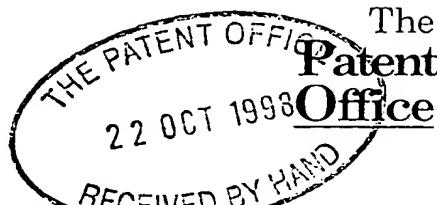
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1. Your reference	S-30683/P1		
2. Patent application number <i>(The Patent Office will fill in this part)</i>	<b>9823098.0</b>		
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Patent ADP number <i>(if you know it)</i>			
If the applicant is a corporate body, give the country/state of its incorporation	<b>SWITZERLAND</b> 7125487002		
4. Title of invention	<b>Organic compounds</b>		
5. Name of your agent <i>(If you have one)</i> "Address for service" in the United Kingdom to which all correspondence should be sent <i>(including the postcode)</i>	<b>B.A. YORKE &amp; CO.</b> <b>CHARTERED PATENT AGENTS</b> <b>COOMB HOUSE, 7 ST. JOHN'S ROAD</b> <b>ISLEWORTH</b> <b>MIDDLESEX TW7 6NH</b>		
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Organic Compounds

The present invention relates to vegetative reproduction of plants and plant cells. In particular the invention relates to a method for increasing the probability of vegetative reproduction *in vivo* through seeds or *in vitro* by somatic embryogenesis. Apomictic seeds resulting therefrom, and the plants and progeny obtained through germination of such seeds are further subject matters of the invention.

Vegetative, non-sexual reproduction through seeds also called apomixis, is a genetically controlled reproductive mechanism of plants found in some polyploid non-cultivated species. Two types of apomixis, gametophytic or non-gametophytic, can be distinguished. In gametophytic apomixis - of which there are two types, namely apospory and diplospory - multiple embryo sacs typically lacking antipodal nuclei are formed, or else megasporogenesis in the embryo sac takes place. In non-gametophytic apomixis also called adventitious embryony, a somatic embryo develops directly from the cells of the embryo sac, ovary wall or integuments. Somatic embryos from surrounding cells invade the sexual ovary, one of the somatic embryos out-competes the other somatic embryos and the sexual embryo, and utilizes the produced endosperm.

Engineering apomixis to a controllable, more reproducible trait would provide many advantages in plant improvement and cultivar development in case that sexual plants are available as crosses with the apomictic plant. The Somatic Embryogenesis Receptor Kinase (SERK) is known to be involved in the formation of extraneous embryos from sporophytic cells which can result in apomictic seeds.

Apomixis would provide for true-breeding, seed propagated hybrids. Moreover, apomixis could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilize a desirable gene combination could be eliminated. Apomixis would provide for the use as cultivars of genotypes with unique gene combinations since apomictic genotypes breed true irrespective of heterozygosity. Genes or groups of genes could thus be "pyramided and "fixed" in super genotypes. Every superior apomictic genotype from a sexual-apomictic cross would have the potential to be a cultivar. Apomixis would allow plant breeders to develop cultivars with specific stable traits for such characters as height, seed and forage quality and maturity.

Breeders would not be limited in their commercial production of hybrids by (i) a cytoplasmic-nuclear interaction to produce male sterile female parents or (ii) the fertility restoring capacity of a pollinator. Almost all cross-compatible germplasm could be a potential parent to produce apomictic hybrids.

Apomixis would also simplify commercial hybrid seed production. In particular, (i) the need for physical isolation of commercial hybrid production fields would be eliminated; (ii) all available land could be used to increase hybrid seed instead of dividing space between pollinators and male sterile lines; and (iii) the need to maintain parental line seed stocks would be eliminated.

The potential benefits to accrue from the production of seed *via* apomixis are presently unrealized, to a large extent because of the problem of engineering apomictic capacity into plants of interest. The present invention teaching introduction of proteins acting in the signal transduction cascade triggered by SERK provides a further step to the solution of that problem in that it improves vegetative reproduction *in vivo* through seeds and *in vitro* by somatic embryogenesis.

In the following the term "gene" refers to a coding sequence and associated regulatory sequences. The coding sequence is transcribed into RNA, which depending on the specific gene, will be mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Examples of regulatory sequences are promoter sequences, 5' and 3' untranslated sequences and termination sequences. Further elements that may be present are, for example, introns.

A "promoter" is a DNA sequence initiating transcription of an associated DNA sequence. Depending on the specific promoter region it may also include elements that act as regulators of gene expression such as activators, enhancers, and/or repressors.

A regulatory DNA sequence such as promoter is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a protein, if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence.

The term "expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants.

Expression "in the vicinity of the embryo sac" is considered to mean expression in carpel, integuments, ovule, ovule premordium, ovary wall, chalaza, nucellus, funicle or placenta. The skilled man will recognize that the term "integuments" can include tissues which are derived therefrom, such as endothelium. "Embryogenic" defines the capability of cells to develop into an embryo under permissive conditions. It will be appreciated that the term "in an active form" includes proteins which are truncated or otherwise mutated with the proviso that they still increase the probability of vegetative reproduction whether or not in doing this they interact with the signal transduction components that they otherwise would in the tissues in which they are normally present.

"Marker genes" encode a selectable or screenable trait. Thus, expression of a "selectable marker gene" gives the cell a selective advantage which may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a plant cell gives the cell both, a negative and a positive selective advantage. On the other hand a "screenable marker gene" does not confer a selective advantage to a transformed cell, but its expression makes the transformed cell phenotypically distinct from untransformed cells.

The term "plant" refers to any plant, but particularly seed plants.

The term "plant cell" describes the structural and physiological unit of the plant, and comprises a protoplast and a cell wall. The plant cell may be in form of an isolated single cell (such as stomatal guard cells) or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

The term "plant material" includes leaves, stems, roots, emerged radicles, flowers or flower parts, petals, fruits, pollen, pollen tubes, anther filaments, ovules, embryo sacs, egg cells, ovaries, zygotes, embryos, zygotic embryos *per se*, somatic embryos, hypocotyl sections,

apical meristems, vascular bundles, pericycles, seeds, cuttings, cell or tissue cultures, or any other part or product of a plant

The following solutions are provided by the present invention:

- A method for increasing the probability of vegetative reproduction of a new plant generation comprising transgenically expressing a gene encoding a protein acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase (SERK);
- said method wherein the encoded protein physically interacts with SERK;
- said method wherein the protein is a member of the family of Squamosa-promoter Binding Protein (SBP) transcription factors or 14-3-3 type lambda proteins;
- said method wherein the protein has the amino acid sequence given in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16, or an amino acid sequence having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% identity with SEQ ID NO: 12 or SEQ ID NO: 16;
- said method increasing the probability of vegetative reproduction through seeds (apomixis);
- said method wherein the seeds result from non-gametophytic apomixis;
- said method wherein the encoded protein is transgenically expressed in the vicinity of the embryo sac;
- said method increasing the probability of *in vitro* somatic embryogenesis;
- said method wherein expression of the gene is under control of the SERK gene promoter, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, The *Arabidopsis* LTP-1 gene promoter, The *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter or the promoter of the O126 gene of *Phalaenopsis*;
- a gene encoding a protein having the amino acid sequence given in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16, or an amino acid sequence having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% sequence identity with SEQ ID NO: 12 or SEQ ID NO: 16;

- said gene having the nucleotide sequence given in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, or SEQ ID NO: 15;
- said gene wherein the nucleotide sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the DNA is to be inserted are used;
- a plant or plant cell transgenically expressing said gene; and
- a plant or plant cell obtainable by the method according to the present invention.

According to the present invention there is provided a method for increasing the probability of vegetative reproduction of a new plant generation, for example by producing apomictic seeds or generating somatic embryos under *in vitro* conditions, comprising transgenically expressing a gene encoding a protein acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase (SERK). This is achieved by

- (i) transforming plant material with a nucleotide sequence encoding said protein,
- (ii) regenerating transformed plant material into plants, or carpel-containing parts thereof, and
- (iii) expressing the sequence in the vicinity of the embryo sac.

A further embodiment of the invention relates to genes encoding proteins acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase (SERK) the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic.

The gene to be expressed preferably encodes a protein physically interacting with SERK. Specific examples of SERK-interacting proteins are members of the family of Squamosa-promoter Binding Protein (SBP) transcription factors (Klein et al, Mol Gen Genet 250: 7-16, 1996). These proteins are able to interact specifically with DNA through a conserved domain of 70 to 90, preferably 79 amino acid residues, the SBP-box. Alignment of different SBP-box sequences generally reveals at least 50% and preferably more than 60% or more than 70 % sequence identity. Within the SBP-box a remarkable arrangement of cysteine and histidine residues can be recognized, which is reminiscent of zinc-fingers and probably involved in the recognition of specific promoter elements. A bipartite nuclear localization signal is placed at the C-terminal end of the SBP-box (Dingwall et al, Trends Biochem Sci 16: 478-481, 1991). Both the N-terminal and the C-terminal domains of the SERK-

- interacting SBP proteins are highly variable and are probably involved in regulation of protein activity. One of the possible SBP proteins is identical with SPL3 (SEQ ID NO: 5 and SEQ ID NO: 6), a gene involved in the floral transition and expressed in developing flower buds (Cardon et al, Plant Journal 12: 367-377, 1997).
- Another class of SERK-interacting proteins are isoforms of the family of 14-3-3 proteins such as the 14-3-3 type lambda protein (Wu et al, Plant Physiol 114: 1421-1431, 1997; SEQ ID NO: 9 and SEQ ID NO: 10). A total of 10 different 14-3-3 proteins are present in *Arabidopsis* the different members being involved in intracellular signal transduction. They mediate signal transduction by binding to phosphoserine-containing proteins on specific binding motifs represented by conserved amino acid sequences like RxxS(p)xP (Yaffe et al, Cell 91: 961-971, 1997). A putative 14-3-3 interaction domain having the amino acid sequence RPPSQP is also found at position 391-396 of the *Arabidopsis* SERK protein, and at the corresponding aligned region of the *Daucus carota* SERK protein having the amino acid sequence RQPSEP providing SERK with a mechanism for a 14-3-3 mediated signal transduction.
- A further class of SERK-interacting proteins is exemplified by SEQ ID NO: 11 (and SEQ ID NO: 12) and the NDR1 protein already described in the literature (Century et al, Science 278: 1963-1965, 1997). NDR1 is likely to encode a membrane-associated component in the signal transduction pathway downstream of pathogen-recognizing proteins. It was suggested that NDR1 might be a protein that interacts with many different receptors. SEQ ID NO: 6 represents a new member in this small family of proteins supposed to function in intracellular signal transduction mediated by transmembrane receptors.
- SEQ ID NO: 13 encodes a SERK-interacting protein (SEQ ID NO: 14) with homology to a domain of *E.coli* aminopeptidase N and is expected to encode an *Arabidopsis* protease interacting with or activated by SERK.
- The predicted amino acid sequence of the SERK-interacting protein of SEQ ID NO: 15 (SEQ ID NO: 16) has no homology with known gene products although there is a small not yet described family of related gene products in *Arabidopsis*.
- Insofar as the the SERK-interacting proteins mentioned above and their corresponding genes are novel they constitute a further subject matter of the present invention.

Of course, genes similar to the ones described above can also be used. A similar gene is a gene having a nucleotide sequence complementary to the test sequence and capable of hybridizing to the inventive sequence. When the test and inventive sequences are double stranded the

nucleic acid constituting the test sequence preferably has a TM within 20°C of that of the inventive sequence. In the case that the test and inventive sequences are mixed together and denatured simultaneously, the TM values of the sequences are preferably within 10°C of each other. More preferably the hybridization is performed under stringent conditions, with either the test or inventive DNA preferably being supported. Thus either a denatured test or inventive sequence is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of between 50° and 70°C in double strength citrate buffered saline (SSC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SSC concentration. Depending upon the degree of stringency required, and thus the degree of similarity of the sequences, at a particular temperature, - such as 60°C, for example - such reduced concentration buffers are typically single strength SSC containing 0.1% SDS, half strength SSC containing 0.1% SDS and one tenth strength SSC containing 0.1% SDS. Sequences having the greatest degree of similarity are those the hybridization of which is least affected by washing in buffers of reduced concentration. It is most preferred that the test and inventive sequences are so similar that the hybridization between them is substantially unaffected by washing or incubation in one tenth strength sodium citrate buffer containing 0.1% SDS.

The gene to be expressed may be modified in that known mRNA instability motifs or polyadenylation signals are removed or codons which are preferred by the plant into which the sequence is to be inserted may be used so that expression of the thus modified sequence in the said plant may yield substantially similar protein to that obtained by expression of the unmodified sequence in the organism in which the protein is endogenous.

The sequence variability of proteins with similar function suggests, that a number of amino acids can be replaced, inserted or deleted without altering a protein's function. The relationship between proteins is reflected by the degree of sequence identity between aligned amino acid sequences of individual proteins or aligned component sequences thereof.

Dynamic programming algorithms yield different kinds of alignments. In general there exist two approaches towards sequence alignment. Algorithms as proposed by Needleman and Wunsch and by Sellers align the entire length of two sequences providing a global alignment of the sequences. The Smith-Waterman algorithm on the other hand yields local alignments. A local alignment aligns the pair of regions within the sequences that are most

similar given the choice of scoring matrix and gap penalties. This allows a database search to focus on the most highly conserved regions of the sequences. It also allows similar domains within sequences to be identified. To speed up alignments using the Smith-Waterman algorithm both BLAST (Basic Local Alignment Search Tool) and FASTA place additional restrictions on the alignments.

Within the context of the present invention alignments are conveniently performed using BLAST, a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. Version BLAST 2.0 (Gapped BLAST) of this search tool has been made publicly available on the internet (currently <http://www.ncbi.nlm.nih.gov/BLAST/>). It uses a heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions. The scores assigned in a BLAST search have a well-defined statistical interpretation. Particularly useful within the scope of the present invention are the blastp program allowing for the introduction of gaps in the local sequence alignments and the PSI-BLAST program, both programs comparing an amino acid query sequence against a protein sequence database, as well as a blastp variant program allowing local alignment of two sequences only. Said programs are preferably run with optional parameters set to the default values.

Sequence alignments using BLAST can also take into account whether the substitution of one amino acid for another is likely to conserve the physical and chemical properties necessary to maintain the structure and function of a protein or is more likely to disrupt essential structural and functional features. For example non-conservative replacements may occur at a low frequency and conservative replacements may be made between amino acids within the following groups:

- (i) Serine and Threonine;
- (ii) Glutamic acid and Aspartic acid;
- (iii) Arginine and Lysine;
- (iv) Asparagine and Glutamine;
- (v) Isoleucine, Leucine, Valine and Methionine;
- (vi) Phenylalanine, Tyrosine and Tryptophan
- (vii) Alanine and Glycine.

Such sequence similarity is quantified in terms of a percentage of positive amino acids, as compared to the percentage of identical amino acids and can help assigning a protein to the correct protein family in border-line cases.

Specific embodiments of the invention express a gene comprising a DNA sequence encoding a protein acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase (SERK) and having the amino acid sequence depicted in SEQ ID NO: 2, 4, 6 or 8, or a protein similar thereto. By similar is meant a protein having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% and preferably 50% or more sequence identity with another protein.

In order to obtain expression of the sequence in a regenerated plant and in particular the carpel thereof in a tissue specific manner the sequence is under expression control of an inducible or developmentally regulated promoter. It is preferred that the gene is expressed in the somatic cells of the embryo sac, ovary wall, nucellus, or integuments. As the endosperm within the apomictic seed results from fusion of polar nuclei within the embryo sac with a pollen-derived male gamete nucleus it is preferred that the sequence encoding the protein is expressed prior to fusion of the polar nuclei with the male gamete nucleus.

Typically promoters are a promoter which regulates expression of SERK genes *in planta*, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 and fbp-11 gene promoters, the *Arabidopsis* AtDMC1 promoter, the pTA7001 inducible promoter. The DcEP3-1 gene is expressed transiently during inner integument degradation and later in cells that line the inner part of the developing endosperm. The AtChitIV gene is transiently expressed in the micropylar endosperm up to cellularisation. The LTP-1 promoter is active in the epidermis of the developing nucellus, both integuments, seed coat and early embryo. The bel-1 gene is expressed in the developing inner integument and the fbp-7 promoter is active during embryo sac development. The *Arabidopsis* ANT gene is expressed during integument development, and the O126 gene from *Phalaenopsis* is expressed in the mature ovule.

The promoters of the DcEP3-1 and the AtChit IV genes may be cloned and characterized by standard procedures. The gene encoding a protein of the SERK signal cascade is cloned behind the DcEP3-1, the AtChit IV or the AtLTP-1 promoters and transformed into *Arabidopsis*.

The ligation is performed in such a way that the promoter is operably linked to the sequence to be transcribed. This construct, which also contains known marker genes providing for selection of transformed material, is inserted into the T-DNA region of a binary vector such as pBIN19 and transformed into *Arabidopsis*. *Agrobacterium*-mediated transformation into *Arabidopsis* is performed by the vacuum infiltration or root transformation procedures known to the skilled man. Transformed seeds are selected and harvested and (where possible) transformed lines are established by normal selfing. Parallel transformations with 35S promoter constructs and the entire SERK-interacting gene itself are used as controls to evaluate over-expression in many cells or only in the few cells that naturally express the gene. The 35S promoter construct may give embryo formation wherever the signal that activates SERK-mediated transduction is present in the plant. A testing system based on emasculation and the generation of donor plant lines for pollen carrying LTP1 promoter-GUS and SERK promoter-barnase is established.

The same constructs (35S, EP3-1, AtChitIV, AtLTP-1 and SERK promoters fused to SERK-interacting coding sequences) can be employed for transformation into several *Arabidopsis* backgrounds such as wild type, male sterile, fis (allelic to emb 173) and primordia timing (pt)-1 lines, or a combination of two or several of these backgrounds. The wt lines are used as a control to evaluate possible effects on normal zygotic embryogenesis, and to score for seed set without fertilization after emasculation. The ms lines are used to score directly for seed set without fertilization. The fis lines exhibit a certain degree of seed and embryo development without fertilization, so may be expected to have a natural tendency for apomictic embryogenesis, which may be enhanced by the presence of the constructs. The pt-1 line has superior regenerative capabilities and has been used to initiate the first stably embryogenic *Arabidopsis* cell suspension cultures. Combinations of several of the above backgrounds are obtained by crossing with each other and with lines expressing SERK-interacting proteins ectopically. Except for the ms lines, propagation can proceed by normal selfing, and analysis of apomictic traits. A similar strategy is followed if the ATChitIV, AtLTP-1 and SERK promoters are replaced by the bel-1 and fbp-7 promoters as well by other promoters specific for components of the female gametophyte.

The invention still further includes vectors comprising DNA as indicated in the preceding paragraphs, plants transformed with the vector, progeny of such plants which contain the DNA stably incorporated, and the apomictic seeds of such plants or such progeny.

The genes to be expressed can be introduced into the plant cells in a number of art-recognized ways summarized in the paragraph bridging pages 7 and 8 of WO 97/43427.

Comprised within the scope of the present invention are transgenic plants, in particular transgenic fertile plants transformed by means of the aforescribed processes and their asexual and/or sexual progeny, which still contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny. Said plants can be used in the same way as described on pages 10 to 12 of WO 97/43427.

A transgenic plant according to the invention may be a dicotyledonous or a monocotyledonous plant. Such plants include field crops, vegetables and fruits including tomato, pepper, melon, lettuce, cauliflower, broccoli, cabbage, brussels sprout, sugar beet, corn, sweetcorn, onion, carrot, leek, cucumber, tobacco, alfalfa, aubergine, beet, broad bean, celery, chicory, cow pea, endive, gourd, groundnut, papaya, pea, peanut, pineapple, potato, safflower, snap bean, soybean, spinach, squashes, sunflower, sorghum, water-melon, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. In a preferred embodiment, the DNA is expressed in "seed crops" such as corn, sweet corn and peas etc. in such a way that the apomictic seed which results from such expression is not physically mutated or otherwise damaged in comparison with seed from untransformed like crops. Preferred are monocotyledonous plants of the *Graminaceae* family involving Lolium, Zea, Triticum, Triticale, Sorghum, Saccharum, Bromus, Oryzae, Avena, Hordeum, Secale and Setaria plants.

More preferred are transgenic maize, wheat, barley, sorghum, rye, oats, turf and forage grasses, millet, rice and sugar cane. Especially preferred are maize, wheat, sorghum, rye, oats, turf grasses and rice.

Among the dicotyledonous plants *Arabidopsis*, soybean, cotton, sugar beet, oilseed rape, tobacco and sunflower are more preferred herein. Especially preferred are tomato, pepper, melon lettuce, *Brassica* vegetables, soybean, cotton, tobacco, sugar beet and oilseed rape.

The expression 'progeny' is understood to embrace both, "asexually" and "sexually" generated progeny of transgenic plants. This definition is also meant to include all mutants and variants obtainable by means of known processes, such as for example cell fusion or mutant selection and which still exhibit the characteristic properties of the initial transformed plant, together with all crossing and fusion products of the transformed plant material. This also includes progeny plants that result from a backcrossing, as long as the said progeny plants still contain the DNA according to the invention.

Another object of the invention concerns proliferation material of the transgenic plants. It is defined relative to the invention as any plant material that may be propagated sexually or asexually *in vivo* or *in vitro*. Particularly preferred within the scope of the present invention are protoplasts, cells, calli, tissues, organs, seeds, embryos, pollen, egg cells, zygotes, together with any other propagating material obtained from transgenic plants.

Parts of plants, such as for example flowers, stems, fruits, leaves, roots originating in transgenic plants or their progeny previously transformed by means of the process of the invention and therefore consisting at least in part of transgenic cells, are also an object of the present invention. Especially preferred are apomictic seeds.

The present invention is exemplified by transgenic expression of a SERK-interacting gene in *Arabidopsis* under the control of plant expression signals, particularly a promoter which regulates expression of SERK genes *in planta*, but preferably a developmentally regulated or inducible promoter such as, for example, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, or the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* AtDMC1 promoter, or the pTA7001 inducible promoter.

The promoters of the DcEP3-1 and the AtChit IV genes may be cloned and characterized by standard procedures. The desired coding sequence is cloned behind the DcEP3-1, the AtChit IV or the AtLTP-1 promoters and transformed into *Arabidopsis*. The ligation is performed in such a way that the promoter is operably linked to the sequence to be transcribed. This construct, which also contains known marker genes providing for selection of transformed material, is inserted into the T-DNA region of a binary vector such as pBIN19 and transformed into *Arabidopsis*. *Agrobacterium*-mediated transformation into *Arabidopsis* is performed by the

vacuum infiltration or root transformation procedures known to the skilled man. Transformed seeds are selected and harvested and (where possible) transformed lines are established by normal selfing. Parallel transformations with 35S promoter constructs and the entire SERK-interacting gene itself are used as controls to evaluate over-expression in many cells or only in the few cells that naturally express the gene. The 35S promoter construct may give embryo formation wherever the signal that activates SERK-mediated transduction is present in the plant. A testing system based on emasculation and the generation of donor plant lines for pollen carrying LTP1 promoter-GUS and SERK promoter-barnase is established.

The same constructs (35S, EP3-1, AtChitIV, AtLTP-1 and SERK promoters fused to the SERK-interacting coding sequence) are employed for transformation into several *Arabidopsis* backgrounds. These backgrounds are wild type, male sterile, fis (allelic to emb 173) and primordia timing (pt)-1 lines, or a combination of two or several of these backgrounds. The wt lines are used as a control to evaluate possible effects on normal zygotic embryogenesis, and to score for seed set without fertilization after emasculation. The ms lines are used to score directly for seed set without fertilization. The fis lines exhibit a certain degree of seed and embryo development without fertilization, so may be expected to have a natural tendency for apomictic embryogenesis, which may be enhanced by the presence of the constructs. The pt-1 line has superior regenerative capabilities and has been used to initiate the first stably embryogenic *Arabidopsis* cell suspension cultures. Combinations of several of the above backgrounds are obtained by crossing with each other and with lines expressing SERK-interacting proteins ectopically. Except for the ms lines, propagation can proceed by normal selfing, and analysis of apomictic traits. A similar strategy is followed in which the ATChitIV, AtLTP-1 and SERK promoters are replaced by the bel-1 and fbp-7 promoters as well by other promoters specific for components of the female gametophyte.

Whilst the present invention has been particularly described by way of the production of apomictic seed by heterologous expression of a SERK-interacting gene in the nucellar region of the carpel, the skilled man will recognize that other genes, the products of which have a similar structure/function may likewise be expressed with similar results. Moreover, although the example illustrates apomictic seed production in *Arabidopsis*, the invention is, of course, not limited to the expression of apomictic seed-inducing genes solely in this plant. Moreover, the present disclosure also includes the possibility of expressing the inventive gene sequences in

transformed plant material in a constitutive, tissue non-specific manner, for example under transcriptional control of a CaMV35S or NOS promoter.

The skilled man who has the benefit of the present disclosure will also recognize that a SERK-interacting genes may be transformed into plant material which may be propagated and/or differentiated and used as an explant from which somatic embryos can be obtained. Expression of such sequences in the transformed tissue substantially increases the percentage of the cells in the tissue which are competent to form somatic embryos, in comparison with the number present in non-transformed like tissue.

The following examples illustrate the isolation and cloning of genes encoding SERK-interacting proteins and the production of apomictic seed by heterologous expression of said genes in the nucellar region of the carpel so that somatic embryos form which penetrate the embryo sac and are encapsulated by the seed as it develops.

## EXAMPLES

### **Example 1: *Isolation of Arabidopsis genes encoding proteins interacting with the Arabidopsis SERK gene product***

#### Construction of a SERK bait plasmid

The cDNA sequence of *Arabidopsis* SERK clone AtSERKtot61 in pBluescript SK- is used as the DNA template to amplify by PCR the SERK open reading frame devoid of its N-terminal sequence using the oligonucleotide primers

V6 (5' -ATGCTTGATAACTTGAGG-3'; SEQ ID NO: 17) and

T7 (5' -AATACGACTCACTATAG-3'; SEQ ID NO: 18).

The resulting PCR product is cloned into the vector pGEM-T (Promega). From the resulting plasmid an Ncol-NotI fragment is isolated and cloned into the Ncol-NotI sites of the yeast *lexA* two hybrid bait vector pEG202 SERK (Origene). Nucleotide sequence analysis is performed to confirm the correct orientation and sequence of the PCR product in the resulting SERK bait plasmid. Bait protein expression and activity is determined using along the protocols described in Current Protocols in Molecular Biology 1996, chapter 20, supplement 33, contributed by E.A. Golemis; J. Gyuris and R. Brent. The construct is shown

to possess transcriptional activity in yeast strain EGY48. Furthermore, repressor activity on a reporter gene shows correct nuclear localization of the SERK gene product. Yeast transformed with the SERK bait plasmid proves to be leucine heterotrophic, indicating that the construct is not resulting in autoactivation of the lexA selection screen. The tests demonstrate that the SERK bait construct is suitable for lexA two hybrid screening.

#### Screening of a lexA two hybrid library

Yeast strain EGY48 transformed with the LacZ reporter plasmid pSH18-34 (Origene) and the bait vector pEG202 SERK is transformed with the cDNA library vector pJG4-5 (Origene) according to the LiAc/PEG4000 procedure described in Current protocols in Molecular Biology 1996, chapter 20, supplement 33, contributed by E.A. Golemis; J. Gyuris and R. Brent. A cDNA library from *Arabidopsis thaliana* young silique tissue containing early globular stage embryos is obtained (provided by Prof. Gerd Jürgens, Tuebingen). The primary library contains approximately 2.000.000 cDNA clones and the average insert length is 1.4 kB (as calculated from 90 clones of which the insert length varies from 0.2 to 4.5 kB). 10% of the clones contain no insert. The library is amplified once in E.coli before screening for SERK protein interaction. Induction of the fusion proteins in pJG4-5 is by the application of galactose in the medium. Under non-inducing conditions, yeast cells are grown in glucose and do not express the pJG4-5 fusion proteins. 4.200.000 prey cDNA clones are transformed into the yeast strain containing the pEG202 SERK bait plasmid and the pSH18-34 reporter plasmid. Transformation efficiency is up to 270.000 colonies per microgram of vector DNA. The plasmid pJG4-5 contains the *TRP1* selectable marker, pSH18-34 has an *URA3* selectable marker and pEG202 contains a *HIS3* selectable marker. Growth of the transformed yeast cells is taking place in complete minimal (CM) medium supplemented with either 2% glucose or 2% galactose + raffinose (in the latter case the galactose-inducible promoter on the vector pJG4-5 is activated, resulting in expression of the cDNA library fusion proteins). Yeast strain EGY48 contains six *LexA* operators which direct transcription from the *LEU2* gene. When both the SERK fusion protein and the cDNA library fusion protein are expressed the LexA DNA-binding domain of the SERK fusion protein can interact with the activation domain of the library cDNA fusion protein to form an active LexA transcription factor which in turn allows to select for leucine autotrophic transformants. The LacZ reporter construct on the plasmid pSH18-34 contains one LexA

operator in a promoter context different from the *LEU2* gene. Xgal and the presence of an active LexA transcription complex also allows determination of LacZ activity.

Triple selection for all three plasmids is performed on GLU/CM-his-ura-trp 24cm/24cm plates with approximately 100.000 colonies per plate. A total of 4.200.000 yeast primary transformants are obtained. The colonies are scraped from the plates with a sterile glass slide, collected in two different A or B labeled 50 ml tubes and frozen at -80°C. In order to estimate the colony titer a sample is plated on GAL/RAF/CM -ura-his-trp-leu plates. After determining the titer, library screening is continued by plating approximately 1.000.000 colonies on 10cm/10cm plates each. A total of 36.000.000 colonies is plated on leu selection plates GAL/CM-his-ura-trp-leu (20 million from vial A and 16 million from vial B). Colonies are isolated when the diameter of the colonies is at least 1+mm. The numbers of isolated colonies from each day and vial are indicated in the tabel below:

2 days	3 days	4 days
15A	93A	27A
9B	81B	25B

All isolated colonies are replated on different plates for determination of LacZ activity and only those colonies are selected which fit to the described criteria for each medium:  
Numbers of isolated colonies from each day and vial are indicated:

GAL/RAF/CM	-ura-his-trp-leu	growth yes
GLU/CM	-ura-his-trp-leu	growth no
GAL/RAF/CM	-ura-his-trp + Xgal	blue and growth yes
GLU/CM	-ura-his-trp + Xgal	not blue, growth yes

<12 hours	20 hours	28 hours	48 hours	72 hours
4A	17A	9A	11A	24A
2B	6B	5B	15B	24B

A total of approximately 250 colonies is growing on leucine selection plates and tested for lacZ activity. 107 of these colonies show blue staining as an indication for lacZ activity.

Colony PCR performed on these 107 colonies with primers around the cloning site of the prey vector pJG4-5 generates approximately 10 different groups of cDNA clones based on PCR size. Sau3A1 digestion of the PCR fragments makes a more detailed grouping of different classes of SERK-interacting candidate cDNA clones possible. Members of all different classes are used to isolate and to clone the prey plasmid into *E.coli* and to determine the nucleotide and predicted amino acid sequence. Prey plasmids are retransformed in yeast and tested for SERK-dependent activation of leu selection and lacZ activity. All classes of cDNA clones prove to display a SERK-dependent yeast LexA two hybrid interaction after retransformation experiments. All these clones represent intracellular or membrane-attached factors involved in the signalling pathway mediated by the SERK receptor kinase protein. A total of 8 different classes of SERK-interacting proteins is identified.

#### Example 2: *Function of SERK-interacting proteins*

Four of the classes of proteins that show an interaction with SERK are members of the family of Squamosa-promoter Binding Protein (SBP) transcription factors (Klein et al, Mol. Gen Genet 250: 7-16, 1996). They are represented by the clones 3A35 (SEQ ID NO: 1 and SEQ ID NO: 2), 3B39 (SEQ ID NO: 3 and SEQ ID NO: 4), 4B19 (SEQ ID NO: 5 and SEQ ID NO: 6), and 3A52 (SEQ ID NO: 7 and SEQ ID NO: 8). These proteins are able to interact specifically with DNA through a conserved domain of 79 amino acid residues, the SBP-box. Within the SBP-box a remarkable arrangement of cysteine and histidine residues can be recognized, which is reminiscent of zinc-fingers and probably involved in the recognition of specific promoter elements. A bipartite nuclear localization signal is placed at the C-terminal end of the SBP-box (Dingwall et al, Trends Biochem Sci 16: 478-481, 1991). Both the N-terminal and the C-terminal domains of the SERK-interacting SBP proteins are highly variable and are probably involved in regulation of protein activity. One of the classes of SBP proteins, represented by 4B19, is identical with SPL3, a gene involved in the floral transition and expressed in developing flower buds (Cardon and Hohmann 1997 Plant Journal 12, 367-377). The most likely model for the signalling pathway mediated by the SERK and SBP proteins is transphosphorylation of cytoplasmic SBP-transcription factors by SERK after ligand binding, followed by nuclear translocation of the factors and binding to specific regulatory DNA target sites on the genome. A similar mode of signal transduction

has been described for animal serine-threonine receptor-kinase proteins which are known to transphosphorylate a family of so called SMAD transcription factors. Phosphorylated activated SMAD proteins are translocated into the nucleus (Heldin et al, Nature 390: 465-471, 1997).

Another class of SERK-interacting proteins is represented by an isoform of the family of 14-3-3 proteins. 4B11 (SEQ ID NO: 9 and SEQ ID NO: 10) is identical to the 14-3-3 type lambda protein (Wu et al, Plant Physiol 114: 1421-1431, 1997). A total of 10 different 14-3-3 proteins is present in *Arabidopsis* and the different members are involved in intracellular signal transduction. They mediate signal transduction by binding to phosphoserine-containing proteins on specific binding motifs represented by conserved amino acid sequences like RxxS(p)xP (Yaffe et al, Cell 91: 961-971, 1997). A putative 14-3-3 interaction domain having the amino acid sequence RPPSQP is also found at position 391-396 of the *Arabidopsis* SERK protein, and at the corresponding aligned region of the *Daucus carota* SERK protein having the amino acid sequence RQPSEP providing SERK with a mechanism for a 14-3-3 mediated signal transduction.

4A24 (SEQ ID NO: 11 and SEQ ID NO: 12) represents a member of a small new *Arabidopsis* gene family from which one member has already been described in the literature as the NDR1 protein (Century et al, Science 278: 1963-1965, 1997). NDR1 is likely to encode a membrane-associated component in the signal transduction pathway downstream of pathogen-recognizing proteins. It was suggested that NDR1 is a protein that interacts with many different receptors to transduce their signal. 4A24 represents a new member in this small family of proteins and might have an important function in intracellular signal transduction mediated by transmembrane receptors.

Clone 3B76 (SEQ ID NO: 13 and SEQ ID NO: 14) encodes a protein with homology to a domain in *E.coli* aminopeptidase N. and might encode an *Arabidopsis* protease, interacting or activated by SERK.

The predicted amino acid sequence represented by clone 4A5 (SEQ ID NO: 15 and SEQ ID NO: 16) has no homology with known gene products although there is a small not yet described family of related gene products in *Arabidopsis* (AA585806, AA651106, T45539).

**Example 3: Transformation of *Arabidopsis* with genes encoding SERK-interacting proteins**

Plasmids containing promoter sequences

- The CaMV 35S promoter enhanced by duplication of the -343 to -90 region (Kay et al, Science 236: 1299-1302, 1987) is isolated from the mMON999 vector by digestion with HindIII and SstI and cloned into the pBluescript SK- vector resulting in vector pMT120.
- The promoter of the FBP7 gene from *Petunia* (Angenent et al, Plant Cell 7: 1569-1582, 1995) is cloned by subcloning the 0.6 kb HindIII-XbaI genomic DNA fragment of FBP7 into the HindIII-XbaI site of pBluescript KS- resulting in the vector FBP201.

Plasmids containing full length SERK-interacting cDNA clones

Full length cDNA of the identified SERK-interacting gene products is produced by RT-PCR amplification of early stage *Arabidopsis* siliques RNA. Full length cDNA is isolated from clones 3A35, 3A52, and 4B19. Clone 3B39 was already present as a full length cDNA clone. Oligo sequences are based on the nucleotide sequences from identical BAC or EST clones.

Binary vector constructs

Based on the pBIN19 vector, a binary vector is constructed for transformation of the *Arabidopsis thaliana* SERK-interacting cDNA under the control of different promoters. The full length cDNA clones of the putative SBP-transcription factors interacting with SERK are blunted by Klenow treatment and cloned into the SmaI site of pBIN19. The polyadenylation sequence from the pea rbcS::E9 gene (Millar et al, Plant Cell 4: 1075-1087, 1992) is placed downstream from the coding sequence by cloning a Klenow-filled EcoRI-HindIII E9 DNA fragment into the Klenow-filled XmaI site of the pBIN19:SERK interacting factor in order to generate the binary vectors pAt3A35, pAt3A52, pAt4B19 and pAt3B39. The pAt binary vectors are used to generate promoter-SERK interacting factor constructs.

- The CaMV 35S promoter is cloned in the SmaI site of the pAt vector constructs as a Klenow-filled KpnI-SstI fragment to give p35SAt vectors.
- The SacI-KpnI fragment of FBP201 is filled with Klenow and cloned into the SmaI site of the pAt vector constructs to give the pFBP201At vectors.

Introduction of plant expression vectors into *Arabidopsis thaliana* plants

The above described vector constructs are electrotransformed into *Agrobacterium tumifaciens* strain C58C1. Wild type *Arabidopsis thaliana* WS plants are grown under standard long day conditions (16 hours light and 8 hours dark). The first emerging inflorescence is removed in order to increase the number of inflorescences. Five days later, plants are used for the vacuum infiltration procedure. Transformed *Agrobacterium* C58C1 is grown on LB plates with 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. Single colonies are used to inoculate 500 ml of liquid medium (as described above) and grown O/N at 28°C. Log phase culture ( $OD_{600}=0.8$ ) is centrifuged to pellet cells and resuspended in 150 ml of infiltration medium (0.5 x MS medium pH 5.7, 5% sucrose and 1 mg/l benzylaminopurine). The inflorescences of 6 *Arabidopsis* plants are submerged in the infiltration suspension while the remaining parts of the plants (which are still potted) are placed upside down on meshed wire to avoid contact with the infiltration medium. Vacuum is applied to the whole set-up for 10 min at 50 kPa. Plants are directly afterwards placed under standard long day conditions. After completed seed setting the seeds are surface sterilized by an 1% sodium hypochlorite soak, thoroughly washed with sterile water and planted onto petridishes with 0.5 x MS medium, 1% agar and 80 mg/l kanamycin in order to select for transformed seeds. After 7 days of germination under long day conditions (10.000 lux) the transformed seedlings can be identified by their green colour of their cotyledons and the appearance of the first true leaves. Transformed seedlings are further grown in soil under long day conditions. The vacuum infiltration method results in approximately 0.1% transformed seeds.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: NOVARTIS AG
- (B) STREET: Schwarzwaldallee 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4058
- (G) TELEPHONE: +41 61 324 11 11
- (H) TELEFAX: + 41 61 322 75 32

(ii) TITLE OF INVENTION: Organic Compounds

(iii) NUMBER OF SEQUENCES: 18

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: 3A35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACGTGTCCGT GGAGGCGGGT CGGGTCAGTC GGGTCAGATA CCAAGGTGCC AAGTGGAGG	60
TTGTGGGATG GATCTAACCA ATGCAAAAGG TTATTACTCG AGACACCGAG TTTGTGGAGT	120
GCACTCTAAA ACACCTAAAG TCACTGTGGC TGGTATCGAA CAGAGGTTTT GTCAACAGTG	180
CAGCAGGTTT CATCAGCTTC CGGAATTGAA CCTAGAGAAA AGGAGTTGCC GCAGGAGACT	240

CGCTGGTCAT AATGAGCGAC GAAGGAAGCC ACAGCCTGCG TCTCTCTCTG TGTTAGCTTC	300
TCGTTACGGG AGGATCGCAC CTTCGCTTTA CGAAAATGGT GATGCTGGAA TGAATGGAAG	360
CTTTCTTGGG AACCAAGAGA TAGGATGGCC AAGTCAAGA ACATTGGATA CAAGAGTGAT	420
GAGGCGGCCA GTGTCATCAC CGTCATGGCA GATCAATCCA ATGAATGTAT TTAGTCAAGG	480
TTCAGTTGGT GGAGGAAGGA CAAGCTCTC ATCTCCAGAG ATTATGGACA CTAAACTAGA	540
GAGCTACAAG G	551

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: 3A35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Glu Met Gly Ser Asn Ser Gly Pro Gly His Gly Pro Gly Gln Ala			
1	5	10	15

Glu Ser Gly Gly Ser Ser Thr Glu Ser Ser Ser Phe Ser Gly Gly Leu		
20	25	30

Met Phe Gly Gln Lys Ile Tyr Phe Glu Asp Gly Gly Gly Ser Gly		
35	40	45

Ser Ser Ser Ser Gly Gly Arg Ser Asn Arg Arg Val Arg Gly Gly Gly		
50	55	60

Ser Gly Gln Ser Gly Gln Ile Pro Arg Cys Gln Val Glu Gly Cys Gly			
65	70	75	80

Met Asp Leu Thr Asn Ala Lys Gly Tyr Tyr Ser Arg His Arg Val Cys		
85	90	95

Gly Val His Ser Lys Thr Pro Lys Val Thr Val Ala Gly Ile Glu Gln

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100	105	110
Arg Phe Cys Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe Asp		
115	120	125
Leu Glu Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg		
130	135	140
Arg Arg Lys Pro Gln Pro Ala Ser Leu Ser Val Leu Ala Ser Arg Tyr		
145	150	155
Gly Arg Ile Ala Pro Ser Leu Tyr Glu Asn Gly Asp Ala Gly Met Asn		
165	170	175
Gly Ser Phe Leu Gly Asn Gln Glu Ile Gly Trp Pro Ser Ser Arg Thr		
180	185	190
Leu Asp Thr Arg Val Met Arg Arg Pro Val Ser Ser Pro Ser Trp Gln		
195	200	205
Ile Asn Pro Met Asn Val Phe Ser Gln Gly Ser Val Gly Gly Arg		
210	215	220
Thr Ser Phe Ser Ser Pro Glu Ile Met Asp Thr Lys Leu Glu Ser Tyr		
225	230	235
Lys Gly Ile Gly Asp Ser Asn Cys Ala Leu Ser Leu Leu Ser Asn Pro		
245	250	255
His Gln Pro His Asp Asn		
260	265	270
Asn Asn Asn Thr Trp Arg Ala Ser Ser Gly Phe Gly Pro Met Thr Val		
275	280	285
Thr Met Ala Gln Pro Pro Pro Ala Pro Ser Gln His Gln Tyr Leu Asn		
290	295	300
Pro Pro Trp Val Phe Lys Asp Asn Asp Asn Asn Asn Met Ser Pro Val Leu		
305	310	315
320		
Asn Leu Gly Arg Tyr Thr Glu Pro Asp Asn Cys Gln Ile Ser Ser Gly		
325	330	335
Thr Ala Met Gly Glu Phe Glu Leu Ser Asp His His His Gln Ser Arg		
340	345	350
Arg Gln Tyr Met Glu Asp Glu Asn Thr Arg Ala Tyr Asp Ser Ser Ser		
355	360	365
His His Thr Asn Trp Ser Leu		
370	375	

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 859 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 3B39

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAACATTGC	TTCCTAACCA	GAAATCCACC	ATCATCTTCC	CACGAATACA	ACTTAAAGCT	60
TTACCAAGAAA	ATGGAGGGTC	AGAGAACACA	ACGCCGGGTT	TACTTGAAAG	ACAAGGCTAC	120
AGTCTCCAAC	CTTGTGAAG	AAGAAATGGA	GAATGGCATG	GATGGAGAAG	AGGAGGATGG	180
AGGAGACGAA	GACAAAAGGA	AGAAGGTGAT	GGAAAGAGTT	AGAGGTCTA	GCACTGACCG	240
TGTTCCATCG	CGACTGTGCC	AGGTCGATAG	GTGCACTGTT	AATTGACTG	AGGCCAAGCA	300
GTATTACCGC	AGACACAGAG	TATGTGAAGT	ACATGCAAAG	GCATCTGCTG	CGACTGTTGC	360
AGGGTCAGG	CAACGCTTTT	GTCAACAATG	CAGCAGGTTT	CATGAGCTAC	CAGAGTTGAA	420
TGAAGCTAAA	AGAACGCTGCA	GGAGGCGCTT	AGCTGGACAC	AATGAGAGGA	GGAGGAAGAT	480
CTCTGGTGAC	AGTTTGAG	AAGGGTCAGG	CCGGAGAGGG	TTTAGCGGTC	AACTGATCCA	540
GACTCAAGAA	AGAACACAGGG	TAGACAGGAA	ACTTCCTATG	ACCAACTCAT	CATTAAAGGG	600
ACACAGATC	AGATAAACCC	TCCCCTCTC	TCTCTCTGT	CATCTACATA	TGCTCTATCT	660
ACACTCTTAT	TAGACAAATA	ATGGCATCTA	ACAATGTCAA	AAAAAGTTGG	TCATGGTATT	720
AAATCCTAGA	GGGAAATATA	AGTATAAACCC	TTTAGTCCCC	TTTATGCTGT	CCTGTAATGA	780
ATATCTATCC	GGAAATGTAT	TCGCATAGTC	TTGCGTCTAA	TAATGTTAT	AAAAAAAAAA	840
AAAAAAAAAA	AAAAAA					859

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3B39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr Leu Lys Asp Lys Ala  
1 5 10 15

Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu Asn Gly Met Asp Gly  
20 25 30

Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg Lys Lys Val Met Glu  
35 40 45

Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro Ser Arg Leu Cys Gln  
50 55 60

Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala Lys Gln Tyr Tyr Arg  
65 70 75 80

Arg His Arg Val Cys Glu Val His Ala Lys Ala Ser Ala Ala Thr Val  
85 90 95

Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Glu  
100 105 110

Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys Arg Arg Arg Leu Ala  
115 120 125

Gly His Asn Glu Arg Arg Lys Ile Ser Gly Asp Ser Phe Gly Glu  
130 135 140

Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu Ile Gln Thr Gln Glu  
145 150 155 160

Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr Asn Ser Ser Phe Lys  
165 170 175

Gly Pro Gln Ile Arg  
180

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Arabidopsis thaliana*
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 4B19

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGAACGAGAA AGGTAAAGCT ACAAGTAGTA GTGGAGTTTG TCAGGTCGAG AGTTGTACCG	60
CGGATATGAG CAAAGCCAAA CAGTACCACA AACGACACAA AGTCTGCCAG TTTCATGCCA	120
AAGCTCCTCA TGTTCCGATC TCTGGTCITC ACCAACGTTT CTGCCAACAA TGCAGCAGGT	180
TTCACGCGCT CAGTGAGTTT GATGAAGCCA AGCGGAGTTG CAGGAGACGC TTAGCTGGAC	240
ACAACGAGAG AAGGCGGAAA AGCACAACTG ACTAAAGACG GTGAAACGTG TGAGATCCCG	300
GTTTGAAGGT TAATGAAACA GGCTTGCTT ACTCTCTCT GTCAGTCTCT TTTAGCTCCT	360
TGTAATCCTC TGTGTCTCTG TCTGTTCTC CATATTACCT GTAATCAAAG CTATCTGCTA	420
AACCTACGAC ATGGTTAAAT AAATGCATTG AGACTTAAAAA AAAAAAAAAA AAAAAAAAAA	479

## (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 4B19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Met Arg Arg Ser Lys Ala Glu Gly Lys Arg Ser Leu Arg Glu  
1 5 10 15

Leu Ser Glu Glu Glu Glu Glu Glu Thr Glu Asp Glu Asp Thr  
20 25 30

Phe Glu Glu Glu Ala Leu Glu Lys Lys Gln Lys Gly Lys Ala Thr  
35 40 45

Ser Ser Ser Gly Val Cys Gln Val Glu Ser Cys Thr Ala Asp Met Ser  
50 55 60

Lys Ala Lys Gln Tyr His Lys Arg His Lys Val Cys Gln Phe His Ala  
65 70 75 80

Lys Ala Pro His Val Arg Ile Ser Gly Leu His Gln Arg Phe Cys Gln  
85 90 95

Gln Cys Ser Arg Phe His Ala Leu Ser Glu Phe Asp Glu Ala Lys Arg  
100 105 110

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Lys Ser  
115 120 125

Thr Thr Asp  
130

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2682 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 3A52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCCATTCAAG GAGACACTAA TGGTGCTCTT ACTTTGAATC TTAATGGTGA AAGTGATGGC	60
CTTTTTCCTG CCAAGAAGAC CAAATCCGGA GCCGTTTGTG AGGTGAAAAA CTGTGAAGCT	120
GATCTTAGTA AAGTTAAGGA TTATCATAGA CGCCATAAGG TCTGTGAGAT GCATTCCAAG	180
GCTACTAGTG CCACTGTCGG AGGTATCTTG CAGCGCTTT GTCAGCAATG TAGTAGGTT	240
CATCTTCTGC CAGGTTTCGA TGACGGAAAG AGAAGTTGTC GTAGACGTTT GGCTGGCCAT	300
AATAAACGTC CGAGGAAAAC AAATCCCGAA CCTGGCGCTA ACGGGAATCC TAGTGATGAT	360
CACTCAAGCA ACTATCTCTT GATTACTCTC TTGAAGATAC TCTCCAATAT GCATAACCAT	420
ACCGGTGATC AAGATTGAT GTCTCATCTT CTGAAGAGCC TCGTAAGGCC TGCTGGCGAA	480
CAGTTAGGGA AAAACITAGT TGAACCTCTT CTACAAGGAG AGATCTCAAG GTTCCTTAAA	540
ATATTGGAAA ACTCCGCTTT GCTTGGGATT GAGCAAGCTC CTCAAGAGGA GTTAAAGCAA	600
TTTCGGCTC GGCAAGATGG GACAGCTACC GAGAACAGAT CAGAAAACA AGTCAAAATG	660
AATGATTITG ATTTGAATGA TATCTATATA GACTCAGATG ACACAGACGT CGAAAGATCT	720
CCTCCTCCAA CGAACCTCAGC GACCAGTTCT CTTGATTATC CTTCATGGAT ACATCAGTCT	780
AGTCCGCCTC AGACAAGTAG GAATTCAAGAT TCAGCATCTG ACCAGTCACC CTCAAGTTCT	840
AGTGAAGATG CTCAGATGCG CACAGGCCGG ATTGTGTC AACTATTGG GAAAGAGCCA	900
AATGAATTTC CTATTGCTT ACGAGGACAG ATTCTTGACT GGTTATCGCA TAGTCCAATC	960
GACATGGAGA GCTACATAAG ACCTGGCTGT ATCGTATTGA CCATCTATCT TCGTCAAGCT	1020
GAAACTGCTT GGGAAAGAACT TTCAGACGAT CTGGGTTITA GCTTAGGGAA GCTCTCTAGAT	1080
CTCTCCGATG ATCCCCTGTG GACAACCTGGA TGGATTATG TAGGGTGCAG AACCAACTTG	1140
CATTITGTATA TAACGGTCAG GTTGTGTTTG ACACCTCATT GTCTCTAAAA AGTCGTGATT	1200
ATAGTCACAT CATTAGCGTT AAACCGCTTG CTATAGCTGC AACGGAGAAG GCTCAATTAA	1260
CAGTTAAAGG CATGAATCTC CGTCGGCGTG GCACAAGGTT ACTTTGTTCT GTTGAAGGAA	1320
AATACTTGAT TCAGGAAACA ACACACGATT CGACGACCAG GGAGGGATGAC GATTCAAGG	1380
ACAACAGTGA GATTGTTGAG TGTGTAAACT TCTCTTGTGA TATGCCTATA TTGAGTGGTC	1440
GAGGATTCAAT GGAGATTGAA GACCAAGGAC TCAGTAGCAG CTTCTTCCTT TTCTTAGTGG	1500
TTGAAGATGA CGATGTTGT TCTGAAATCC GTATACTTGA AACCACATTA GAGTCACTG	1560
GAAC TGCTAAGCAA GCTATGGATT TCATACATGA AATCGGTGG CTTCTTCACA	1620

GAAGTAAACT TGGGAATCA GACCAAATC CAGCGTTTT CCCATTAATA CGCTTCCAGT	1680
GGCTAATCGA GTTCTCAATG GATCGAGAGT GGTGCGCTGT GATCAGAAAG CTATTAAACA	1740
TGTTCITTGTA TGGAGCTGTT GGTGAATTTC CTTCCTCCTC TAATGCCACA CTGTCAGAAC	1800
TGTGCCTCT TCACAGAGCC GTGAGGAAAA ACTCTAAGCC TATGGTIGAA ATGCTCTGTA	1860
GATATATTCC CAAGAACAG AGAAACAGCT TGTTAGACC CGATGCTGCT GGTCCAGCCG	1920
GCTTAACACC TCTTCATATT GCAGCTGGTA AAGACGGTTC AGAAGATGTG TTGGATGCGC	1980
TAACAGAAGA TCCTGCAATG GTGGGGATTG AAGCGTGGAA GACATGTCGA GACAGCACAG	2040
GCTTCACACC AGAAGACTAC GCACGCTTAC GCGGTCACTT CTCATACATC CACTTGATTIC	2100
AACCCAAGAT CAATAAAAAG TCAACAACTG AAGATCATGT TGTGGTCAAC ATCCCAGTTT	2160
CTTTCTCAGA CAGAGAGCAG AAAGAACCAA AATCAGGTCC GATGGCTTCA GCCTTGGAGA	2220
TCACACAGAT TCCATGCAAG CTCTGTGACC ATAAACTGGT GTATGGGACA ACACGCAGGT	2280
CTGTAGCGTA CAGACCAGCT ATGTTGTCAA TGGTGGCGAT TGCTGCGGTT TGCCTCTGTG	2340
TGGCACTTCT GTTTAAGAGT TGCCCGGAAG TGCTCTATGT GTTTCAACCG TTCAGGTGGG	2400
AGTTATTGGA CTATGGAACA AGCTGAGTGT AAGTCTACTT TGAAAGATCT TCTAAGATAT	2460
ATATATGAAT GTTACTTATA TAAAACCATA GAGGTGTGAT TTCTATATGT AACTATATGA	2520
GTATAAGATA TAGAGACATG TTGGAGAAGA AGATTGTTGT TATTATTGTT GTTGTGTTG	2580
TTGTGTAAAA GCCTCTCCTA TCTCTCTCGA ACCTAAGGAT TCTCTCTCTG ATTAGTATAT	2640
TTTTTGTGTTG ACAAAAAAAAAA AAAAAGAAAAA AAAAAGAAAAA AA	2682

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 848 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

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## (B) CLONE: 3A52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Glu	Ala	Arg	Ile	Asp	Glu	Gly	Gly	Glu	Ala	Gln	Gln	Phe	Tyr	Gly
1				5					10				15		
Ser	Val	Gly	Asn	Ser	Ser	Asn	Ser	Ser	Ser	Cys	Ser	Asp	Glu	Gly	
	20					25						30			
Asn	Asp	Lys	Lys	Arg	Arg	Ala	Val	Ala	Ile	Gln	Gly	Asp	Thr	Asn	Gly
		35				40						45			
Ala	Leu	Thr	Leu	Asn	Leu	Asn	Gly	Glu	Ser	Asp	Gly	Leu	Phe	Pro	Ala
	50				55							60			
Lys	Lys	Thr	Lys	Ser	Gly	Ala	Val	Cys	Gln	Val	Glu	Asn	Cys	Glu	Ala
	65				70				75			80			
Asp	Leu	Ser	Lys	Val	Lys	Asp	Tyr	His	Arg	Arg	His	Lys	Val	Cys	Glu
		85				90						95			
Met	His	Ser	Lys	Ala	Thr	Ser	Ala	Thr	Val	Gly	Gly	Ile	Leu	Gln	Arg
		100				105						110			
Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Leu	Leu	Pro	Gly	Phe	Asp	Asp
		115				120						125			
Gly	Lys	Arg	Ser	Cys	Arg	Arg	Arg	Leu	Ala	Gly	His	Asn	Lys	Arg	Pro
		130			135							140			
Arg	Lys	Thr	Asn	Pro	Glu	Pro	Gly	Ala	Asn	Gly	Asn	Pro	Ser	Asp	Asp
	145				150				155			160			
His	Ser	Ser	Asn	Tyr	Leu	Leu	Ile	Thr	Leu	Leu	Lys	Ile	Leu	Ser	Asn
		165				170						175			
Met	His	Asn	His	Thr	Gly	Asp	Gln	Asp	Leu	Met	Ser	His	Leu	Leu	Lys
		180				185						190			
Ser	Leu	Val	Ser	His	Ala	Gly	Glu	Gln	Leu	Gly	Lys	Asn	Leu	Val	Glu
		195				200						205			
Leu	Leu	Leu	Gln	Gly	Arg	Arg	Ser	Gln	Gly	Ser	Leu	Asn	Ile	Gly	Asn
		210			215							220			
Ser	Ala	Leu	Leu	Gly	Ile	Glu	Gln	Ala	Pro	Gln	Glu	Leu	Lys	Gln	
	225				230				235			240			
Phe	Ser	Ala	Arg	Gln	Asp	Gly	Thr	Ala	Thr	Glu	Asn	Arg	Ser	Glu	Lys
		245				250						255			
Gln	Val	Lys	Met	Asn	Asp	Phe	Asp	Leu	Asn	Asp	Ile	Tyr	Ile	Asp	Ser
		260				265						270			

Asp Asp Thr Asp Val Glu Arg Ser Pro Pro Pro Thr Asn Pro Ala Thr  
 275 280 285  
 Ser Ser Leu Asp Tyr Pro Ser Trp Ile His Gln Ser Ser Pro Pro Gln  
 290 295 300 320  
 Thr Ser Arg Asn Ser Asp Ser Ala Ser Asp Gln Ser Pro Ser Ser Ser  
 305 310 315 320  
 Ser Glu Asp Ala Gln Met Arg Thr Gly Arg Ile Val Phe Lys Leu Phe  
 325 330 335  
 Gly Lys Glu Pro Asn Glu Phe Pro Ile Val Leu Arg Gly Gln Ile Leu  
 340 345 350  
 Asp Trp Leu Ser His Ser Pro Thr Asp Met Glu Ser Tyr Ile Arg Pro  
 355 360 365  
 Gly Cys Ile Val Leu Thr Ile Tyr Leu Arg Gln Ala Glu Thr Ala Trp  
 370 375 380  
 Glu Glu Leu Ser Asp Asp Leu Gly Phe Ser Leu Gly Lys Leu Leu Asp  
 385 390 395 400  
 Leu Ser Asp Asp Pro Leu Trp Thr Thr Gly Trp Ile Tyr Val Arg Val  
 405 410 415  
 Gln Asn Gln Leu Ala Phe Val Tyr Asn Gly Gln Val Val Val Asp Thr  
 420 425 430  
 Ser Leu Ser Leu Lys Ser Arg Asp Tyr Ser His Ile Ile Ser Val Lys  
 435 440 445  
 Pro Leu Ala Ile Ala Ala Thr Glu Lys Ala Gln Phe Thr Val Lys Gly  
 450 455 460  
 Met Asn Leu Arg Arg Arg Gly Thr Arg Leu Leu Cys Ser Val Glu Gly  
 465 470 475 480  
 Lys Tyr Leu Ile Gln Glu Thr Thr His Asp Ser Thr Thr Arg Glu Asp  
 485 490 495  
 Asp Asp Phe Lys Asp Asn Ser Glu Ile Val Glu Cys Val Asn Phe Ser  
 500 505 510  
 Cys Asp Met Pro Ile Leu Ser Gly Arg Gly Phe Met Glu Ile Glu Asp  
 515 520 525  
 Gln Gly Leu Ser Ser Ser Phe Phe Pro Phe Leu Val Val Glu Asp Asp  
 530 535 540  
 Asp Val Cys Ser Glu Ile Arg Ile Leu Glu Thr Thr Leu Glu Phe Thr  
 545 550 555 560

Gly Thr Asp Ser Ala Lys Gln Ala Met Asp Phe Ile His Glu Ile Gly  
 565 570 575

Trp Leu Leu His Arg Ser Lys Leu Gly Glu Ser Asp Pro Asn Pro Gly  
 580 585 590

Val Phe Pro Leu Ile Arg Phe Gln Trp Leu Ile Glu Phe Ser Met Asp  
 595 600 605

Arg Glu Trp Cys Ala Val Ile Arg Lys Leu Leu Asn Met Phe Phe Asp  
 610 615 620

Gly Ala Val Gly Glu Phe Ser Ser Ser Asn Ala Thr Leu Ser Glu  
 625 630 635 640

Leu Cys Leu Leu His Arg Ala Val Arg Lys Asn Ser Lys Pro Met Val  
 645 650 655

Glu Met Leu Leu Arg Tyr Ile Pro Lys Gln Gln Arg Asn Ser Leu Phe  
 660 665 670

Arg Pro Asp Ala Ala Gly Pro Ala Gly Leu Thr Pro Leu His Ile Ala  
 675 680 685

Ala Gly Lys Asp Gly Ser Glu Asp Val Leu Asp Ala Leu Thr Glu Asp  
 690 695 700

Pro Ala Met Val Gly Ile Glu Ala Trp Lys Thr Cys Arg Asp Ser Thr  
 705 710 715 720

Gly Phe Thr Pro Glu Asp Tyr Ala Arg Leu Arg Gly His Phe Ser Tyr  
 725 730 735

Ile His Leu Ile Gln Arg Lys Ile Asn Lys Lys Ser Thr Glu Asp  
 740 745 750

His Val Val Val Asn Ile Pro Val Ser Phe Ser Asp Arg Glu Gln Lys  
 755 760 765

Glu Pro Lys Ser Gly Pro Met Ala Ser Ala Leu Glu Ile Thr Gln Ile  
 770 775 780

Pro Cys Lys Leu Cys Asp His Lys Leu Val Tyr Gly Thr Thr Arg Arg  
 785 790 795 800

Ser Val Ala Tyr Arg Pro Ala Met Leu Ser Met Val Ala Ile Ala Ala  
 805 810 815

Val Cys Val Cys Val Ala Leu Leu Phe Lys Ser Cys Pro Glu Val Leu  
 820 825 830

Tyr Val Phe Gln Pro Phe Arg Trp Glu Leu Leu Asp Tyr Gly Thr Ser  
 835 840 845

## (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 576 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Arabidopsis thaliana*
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 4B11

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAGCGGAAGA GCTCACCGTT	GAAGAGAGGA ATCTCCTCTC	TGTTGCTTAC AAAAACGTGA	60	
TCGGATCTCT	ACGCGCCGCC	TGGAGGATCG TGTCTTCGAT	TGAGCAGAAG GAAGAGAGTA	120
GGAAGAACGA	CGAGCACGTG	TCGCTTGTCAGGATTACAG	ATCTAAAGTT GAGTCTGAGC	180
TTTCTCTGT	TTGCTCTGGA	ATCCCTTAAGC TCCTTGACTC	GCATCTGATC CCATCTGCTG	240
GAGCGAGTGA	GTCTAAGGTC	TTTTACTTGA AGATGAAAGG	TGATTATCAT CGGTACATGG	300
CTGAGTTAA	GTCTGGTGT	GAGAGGAAAA CTGCTGCTGA	AGATACCATG CTCGCTTACA	360
AAGCAGCTCA	GGATATCGCA	GCTGCGGATA TGGCACCTAC	TCATCCGATA AGGCTTGGTC	420
TGGCCCTGAA	TTTCTCAGTG	TTCTACTATG AGATTCTCAA	TTCTTCAGAC AAAGCTTGTAA	480
ACATGGCCAA	ACAGGCTTTT	GAGGAAGCCA TAGCTGAGCT	TGACACTCTG GGAGAAGAAT	540
CCTACAAAGA	CAGCACTCTC	ATAATGCAGT TGCTGA		576

## (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 248 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ala Ala Thr Leu Gly Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu  
1 5 10 15

Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln  
20 25 30

Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr Val Glu Glu Arg  
35 40 45

Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala  
50 55 60

Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys  
65 70 75 80

Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu  
85 90 95

Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys Leu Leu Asp Ser  
100 105 110

His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys Val Phe Tyr Leu  
115 120 125

Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu Phe Lys Ser Gly  
130 135 140

Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu Ala Tyr Lys Ala  
145 150 155 160

Ala Gln Asp Ile Ala Ala Asp Met Ala Pro Thr His Pro Ile Arg  
165 170 175

Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn  
180 185 190

Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala Phe Glu Glu Ala  
195 200 205

Ile Ala Glu Leu Asp Thr Leu Gly Glu Ser Tyr Lys Asp Ser Thr  
210 215 220

Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp  
225 230 235 240

Met Gln Glu Gln Met Asp Glu Ala  
245

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A24

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGCCGCCACC	GCGATGTACG	TGATCTACCA	CCCTCGTCCG	CCGTCGTTCT	CCGTCCCCGTC	60
AATAAGAAC	AGCCCGTGA	ACCTAACAAAC	CTCCTCTGAT	TCCTCCGTCT	CTCATCTCTC	120
TTCCCTCTTC	AACTTCACTC	TAATCTCAGA	GAATCCAAAC	CAACACCTCT	CTTTCTCTTA	180
CGATCCTTTC	ACCGTCACCG	TTAATTCAAG	TAAATCCGGT	ACGATGCTCG	GTAACGGAAC	240
TGTTCCCTGCT	TTCCTCAGCG	ATAACGGTAA	CAAAACTTCG	TTTCACGGCG	TGATCGCTAC	300
GTCTACAGCG	GCGCGTGAGT	TAGATCCGGA	TGAAGCTAAG	CATCTGAGAT	CAGATCTGAC	360
GCGCGCGCGT	GTAGGATATG	AGATCGAGAT	GAGAACTAAA	GTGAAGATGA	TAATGGGGAA	420
GCTGAAGAGT	GAAGGAGTAG	AGATCAAAGT	GACATGTTGA	AGGATTGAA	GGAACTATAAC	480
CAAAGGTAA	AACTCCAATT	GTAGCTACTT	CTAAAAAAAC	TAAGTGAAAG	TCTGATCTTA	540
GTGTCAAGTC	TGGAAATGGA	TTTCTAAAGG	AATTGATAA	TTTCACATTG	AAATTCTATA	600
TATCTCTCTT	TTTCTCTGGA	TTTGTGAAAC	TTTGGATGAT	CAAAGAATTC	TTCATTTGTC	659

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4A24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg	Ile	Cys	Cys	Cys	Cys	Phe	Trp	Ser	Ile	Leu	Ile	Ile	Leu	Ile	Leu
1									5					10	15

Ala	Leu	Met	Thr	Ala	Ile	Ala	Ala	Thr	Ala	Met	Tyr	Val	Ile	Tyr	His
									20			25		30	

Pro	Arg	Pro	Pro	Ser	Phe	Ser	Val	Pro	Ser	Ile	Arg	Ile	Ser	Arg	Val
									35			40		45	

Asn	Leu	Thr	Thr	Ser	Ser	Asp	Ser	Ser	Val	Ser	His	Leu	Ser	Ser	Phe
									50			55		60	

Phe	Asn	Phe	Thr	Leu	Ile	Ser	Glu	Asn	Pro	Asn	Gln	His	Leu	Ser	Phe
									65			70		75	80

Ser	Tyr	Asp	Pro	Phe	Thr	Val	Thr	Val	Asn	Ser	Ala	Lys	Ser	Gly	Thr
									85			90		95	

Met	Leu	Gly	Asn	Gly	Thr	Val	Pro	Ala	Phe	Phe	Ser	Asp	Asn	Gly	Asn
									100			105		110	

Lys	Thr	Ser	Phe	His	Gly	Val	Ile	Ala	Thr	Ser	Thr	Ala	Ala	Arg	Glu
									115			120		125	

Leu	Asp	Pro	Asp	Glu	Ala	Lys	His	Leu	Arg	Ser	Asp	Leu	Thr	Arg	Ala
									130			135		140	

Arg	Val	Gly	Tyr	Glu	Ile	Glu	Met	Arg	Thr	Lys	Val	Lys	Met	Ile	Met
									145			150		155	160

Gly	Lys	Leu	Lys	Ser	Glu	Gly	Val	Glu	Ile	Lys	Val	Thr	Cys		
									165			170			

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3B76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCTCCAACTC CAGGCCAGCC AACAAAAGAA CCTACATTAA TTCCAGTGGT TGTGTTCTT	60
TTGGACTCAA GTGGGAAAGA CATTACTCTT TCCTCTGTT ATTATGATGG TACAGTGCAG	120
ACCATTTCAAG GCAGCAGCAC AATACTTCGA GTGACAAGAA ACAAGAAGAG TTTGTGTTTT	180
CTGATATAACC AGAAAGACCT GTTCCGTCCC TATTTAGGGG ATTCAGCCCC AGTTCTGTGTT	240
GAAACTGATC TCTCTAACATGA TGACTTATTC TTCCCTCCTAG CACATGATTC AGATGAATTC	300
AATAGGTGGG AGGCCGGTCA AGTTCTGGCA AGAAAGCTGA TGCTGAACCTT AGTTCTGAT	360
TTCCAGCAAA ATAAACCGTT GGCTCTAAC CCAAAATTG TGCAAGGTCT CGGCAGTGTG	420
CTTTCTGACT CAAGCTTGGGA CAAGGAATTG ATAGCCAAAG CAATAACACT ACCTGGGGAG	480
GGAGAGATAA TGGACATGAT GGCGTGGCG GATCCTGATG CTGTTCATGC TGTTAGAAAG	540
TTTGTACGAA AGCAGCTTGC ATCTGAACCTT AAGGAGGAGC TTCT	584

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 3B76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Pro Pro Thr Pro Gly Gln Pro Thr Lys Glu Pro Thr Phe Ile Pro Val  
1 5 10 15

Val Val Gly Leu Leu Asp Ser Ser Gly Lys Asp Ile Thr Leu Ser Ser  
20 25 30

Val His Tyr Asp Gly Thr Val Gln Thr Ile Thr Gly Ser Ser Thr Ile  
35 40 45

Leu Arg Val Thr Lys Lys Gln Glu Glu Phe Val Phe Ser Asp Ile Pro  
50 55 60

Glu Arg Pro Val Pro Ser Leu Phe Arg Gly Phe Ser Ala Pro Val Arg  
65 70 75 80

Val Glu Thr Asp Leu Ser Asn Asp Asp Leu Phe Phe Leu Leu Ala His  
85 90 95

Asp Ser Asp Glu Phe Asn Arg Trp Glu Ala Gly Gln Val Leu Ala Arg  
100 105 110

Lys Leu Met Leu Asn Leu Val Ser Asp Phe Gln Gln Asn Lys Pro Leu  
115 120 125

Ala Leu Asn Pro Lys Phe Val Gln Gly Leu Gly Ser Val Leu Ser Asp  
130 135 140

Ser Ser Leu Asp Lys Glu Phe Ile Ala Lys Ala Ile Thr Leu Pro Gly  
145 150 155 160

Glu Gly Glu Ile Met Asp Met Met Ala Val Ala Asp Pro Asp Ala Val  
165 170 175

His Ala Val Arg Lys Phe Val Arg Lys Gln Leu Ala Ser Glu Leu Lys  
180 185 190

Glu Glu Leu Lys Ile Val Glu Asn Asn Arg Ser Thr Glu Ala Tyr Val  
195 200 205

Phe Asp His Ser Asn Met Ala Arg Arg Ala Leu Lys Asn Thr Ala Leu  
210 215 220

Ala Tyr Leu Ala Ser Leu Glu Asp Pro Ala Tyr Met Gly Thr Cys Thr  
225 230 235 240

Glu Arg Ile Gln Gly Gly His Gln Phe Asp Arg Pro Ile Cys Cys Phe  
245 250 255

Gly Thr Leu Ser Gln Asn Pro Gly Lys Thr Arg Glu Arg Thr Phe Leu

260

265

270

Pro Asp Phe Tyr Glu Gln Val Ala Gly Thr Ile  
 275                            280

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGGAGGG GAAAAAGTCT TACCCCATGG ACATCCCGGG GATTGAGTGT TACCCGAAAA	60
GGATGAAGAA TGGTATTCTT CCGTCGTGGA CCCCATGCAC CCATTGGAA AGCCGTGTGG	120
CGTTTTCTTT CAGGGATGAT AGAAAAGTGC TCCCTTGGGA TGGAAAGGAG GAGCCTTTAC	180
TGGTAGTGGC CGATAGGGTG AGGAATGTTG TGGAGGCTGA TGACGGGTAT TATCTCGTGG	240
TGGCTGAGAA CGGACTTAAG CTAGAGAAAG GATCAGATTT GAAGGCGAGA GAGGTGAAGG	300
AGAGTTTAGG GATGGTTGTT TTGGTGGTGA GGCGCCAAG AGAAGATGAT GATGATTGGC	360
AGACAAGTCA TCAGAACTGG GACTGAATTA ATAGAATCAA TACTCATATG CTGTAACGTGA	420
TTACGGAGTC ATCATGGTCA TGTAAAATT TTGGATAAAG GTGGTAACIT TTTGTTCTAA	480
GATACAATCA GAAACAGAGC AATATTTTC TCTAAAAAAA AAAAAAAAAA AAAA	534

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asp Ile Pro Gly Ile Glu Cys Tyr Pro Lys Arg Met Lys Asn Gly  
1 5 10 15

Ile Pro Pro Ser Trp Thr Pro Cys Thr His Trp Glu Ser Arg Val Ala  
20 25 30

Phe Ser Phe Arg Asp Asp Arg Lys Val Leu Pro Trp Asp Gly Lys Glu  
35 40 45

Glu Pro Leu Leu Val Val Ala Asp Arg Val Arg Asn Val Val Glu Ala  
50 55 60

Asp Asp Gly Tyr Tyr Leu Val Val Ala Glu Asn Gly Leu Lys Leu Glu  
65 70 75 80

Lys Gly Ser Asp Leu Lys Ala Arg Glu Val Lys Glu Ser Leu Gly Met  
85 90 95

Val Val Leu Val Val Arg Pro Pro Arg Glu Asp Asp Asp Asp Trp Gln  
100 105 110

Thr Ser His Gln Asn Trp Asp  
115

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer V6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGCTTGCA TAACTTGAG G

21

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: primer T7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATACGACTC ACTATAG

17

**What we claim is:**

1. A method for increasing the probability of vegetative reproduction of a new plant generation comprising transgenically expressing a gene encoding a protein acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase (SERK).
2. A method according to claim 1, wherein the encoded protein physically interacts with SERK.
3. The method according to claim 2, wherein the protein is a member of the family of Squamosa-promoter Binding Protein (SBP) transcription factors or 14-3-3 type lambda proteins.
4. The method according to claim 2, wherein the protein has the amino acid sequence given in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16, or an amino acid sequence having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% identity with SEQ ID NO: 12 or SEQ ID NO: 16.
5. The method according to claim 1 increasing the probability of vegetative reproduction through seeds (apomixis).
6. The method according to claim 5, wherein the seeds result from non-gametophytic apomixis.
7. The method according to claim 5, wherein the encoded protein is transgenically expressed in the vicinity of the embryo sac.
8. The method according to claim 1 increasing the probability of *in vitro* somatic embryogenesis.
9. The method according to claim 1, wherein expression of the gene is under control of the SERK gene promoter, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis*

AtChitIV gene promoter, The *Arabidopsis* LTP-1 gene promoter, The *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter or the promoter of the O126 gene of *Phalaenopsis*.

10. A gene encoding a protein having the amino acid sequence given in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16, or an amino acid sequence having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% sequence identity with SEQ ID NO: 12 or SEQ ID NO: 16.
11. A gene according to claim 10 having the nucleotide sequence given in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, or SEQ ID NO: 15.
12. A gene according to claim 10 wherein the nucleotide sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the DNA is to be inserted are used.
13. A plant or plant cell transgenically expressing the gene according to any one of claims 10-12.
14. A plant or plant cell obtainable by the method of claim 1.

